

EXHIBIT B

ClustalW (v1.4) multiple sequence alignment

1. huLGR8-A vs. huLGR8-C

Aligned Length = 754 Gaps = 3
Identities = 681 (90%) Similarities = 0 (0%)

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huLGR8-A   1 MIVFLVFKHLFSLRLITMFFLLHFIVLINVKDFALTQGSMTTPSCQKGYF  50
huLGR8-C   1 MIVFLVFKHLFSLRLITMFFLLHFIVLINVKDFALTQGSMTTPSCQKGYF  50
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huLGR8-A  51 PCGNLTkCLPRAFHCDGKDDCGNGADEENCGDTSGWATIFGTVHGNANSV 100
huLGR8-C  51 PCGNLTkCLPRAFHCDGKDDCGNGADEENCGDTSGWATIFGTVHGNANSV 100
*****

huLGR8-A 101 ALTQECFLKQYPQCCDCKETELECvNGDLKSVPMISNNVTLLSLKKNKIh 150
huLGR8-C 101 ALTQECFLKQYPQCCDCKETELECvNGDLKSVPMISNNVTLLSLKKNKIh 150
*****

huLGR8-A 151 SLPDkVFIKYTKLKKIFLQHNCIRHISRKAffGLCNLQILyLNHNcITTL 200
huLGR8-C 151 SLPDkVFIKYTKLKKIFLQHNCIRHISRKAffGLCNLQIL----- 190
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huLGR8-A 201 RPGIFKDLHQLTWLiLDDNPITRISQRLFTGLNSLFFLSMVNNyLEALPK 250
huLGR8-C 191 -----iLDDNPITRISQRLFTGLNSLFFLSMVNNyLEALPK 226
*****

huLGR8-A 251 QMCAQMPQLNWVDLEGNRIKYLTNSTFLSCDSLTVLFLPRNQIGFVPEKT 300
huLGR8-C 227 QMCAQMPQLNWVDLEGNRIKYLTNSTFLSCDSLTVLDL----- 264
***** *

huLGR8-A 301 FSSLKNLGELDLSSNTITELSPHLFKDLKLLQKLNLSSNPLMyLHKNQFE 350
huLGR8-C 265 -----SSNTITELSPHLFKDLKLLQKL----- 286
*****

huLGR8-A 351 SLKQLQSLDLERIEIPNINTRMFQPMKNLSHIYFKNFRYCSYAPHVRICM 400
huLGR8-C 287 -----DLERIEIPNINTRMFQPMKNLSHIYFKNFRYCSYAPHVRICM 328
*****

huLGR8-A 401 PLTDGISSFEDLLANNILRIFVWVIAFITCFGNLFVIGMRsFIKAENTTH 450
huLGR8-C 329 PLTDGISSFEDLLANNILRIFVWVIAFITCFGNLFVIGMRsFIKAENTTH 378
*****

huLGR8-A 451 AMSIKILCCADCLMGVYLFFVGIFDIKYRGQYQKYALLWMESVQCRLMGF 500
huLGR8-C 379 AMSIKILCCADCLMGVYLFFVGIFDIKYRGQYQKYALLWMESVQCRLMGF 428
*****

huLGR8-A 501 LAMLSTEVSVLLLTYLTLEKFLVIVFPFSNIRPGKRQTSVILICIWMAGF 550
huLGR8-C 429 LAMLSTEVSVLLLTYLTLEKFLVIVFPFSNIRPGKRQTSVILICIWMAGF 478
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huLGR8-A 551 LIAVIPFWNKDYFGNFYgKNGVCFPLYyDQTEDIGSKGYSLGIFLGvNLL 600
huLGR8-C 479 LIAVIPFWNKDYFGNFYgKNGVCFPLYyDQTEDIGSKGYSLGIFLGvNLL 528
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huLGR8-A 601 AFLIIVFSYITMFCSIQKTALQTTEVRNCFGREVAVANRFFFIVFSDAIC 650
huLGR8-C 529 AFLIIVFSYITMFCSIQKTALQTTEVRNCFGREVAVANRFFFIVFSDAIC 578
*****

huLGR8-A 651 WIPVFVVKILSLFRVEIPDTMTSWIVIFFLPVNSALNPILYTLTTNFFKD 700
huLGR8-C 579 WIPVFVVKILSLFRVEIPDTMTSWIVIFFLPVNSALNPILYTLTTNFFKD 628
*****

huLGR8-A 701 KLKQLLHKHQKRSIFKIKKKSLSTSIVWIEDSSSLKLGVLNKITLGDSIM 750
huLGR8-C 629 KLKQLLHKHQKRSIFKIKKKSLSTSIVWIEDSSSLKLGVLNKITLGDSIM 678
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huLGR8-A 751 KPVS 754
huLGR8-C 679 KPVS 682
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